Bovine tuberculosis in Cameroon – putting the pieces together

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The epidemiology of bovine tuberculosis is still poorly understood in sub-Saharan Africa where the prevalence of *Mycobacterium* species in livestock populations is largely unknown. This study aims to estimate the performance of various TB diagnostic tests and use these to estimate the true prevalence of bovine TB in Cameroon and the impacts of co-infections on individual animal risk. This poster describes the three components of the project: (a) an abattoir study, (b) a population based cross sectional study and (c) the laboratory diagnostics.

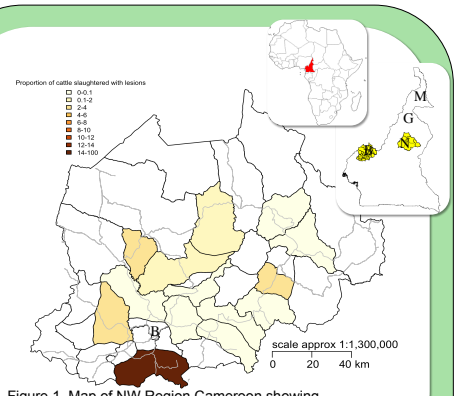
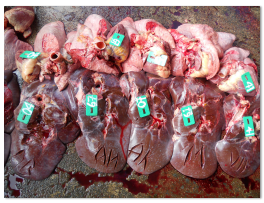


Figure 1. Map of NW Region Cameroon showing subdivision prevalence of lesioned cattle slaughtered in Bamenda abattoir. Inset map of Cameroon showing locations of abattoirs

Abattoir study

Methods: A convenience sample of cattle being slaughtered was taken between 2012–2013 in Bamenda, Ngaoundere, Garoua and Maroua abattoirs (inset Figure 1). Ante mortem examinations and blood samples linked to post mortem meat inspection and clinical material from lesions were collected. Blood samples were screened using the Prionics ® Bovigam and the IDEXX TB Ab ELISAs. Material from all lesioned and a random sample of non-lesioned lymph nodes were sent for culture at the BTRL.

Results: 1129, 756, 170 and 106 slaughtered cattle were examined at the 4 abattoirs respectively. Forty-four (3.9%), 88 (11.6%), 35 (20.6%) and 15 (14.2%) sampled cattle had visible lesions in one or more organs from each site respectively. The distribution of lesioned cattle in the NW Region is shown in Figure 1.



Population based cross-sectional study

Methods: A population based stratified two stage cluster sample of 1500 cattle from 100 georeferenced herds was sampled from the NW Region and the Vina Division of the Adamawa Region (inset Figure 2). Linked examination/ questionnaire data with single comparative intra-dermal tuberculin skin test (SCITT) results and blood samples for IDEXX Ab and Bovigam ELISAs were collected. In addition, these animals will be screened for evidence of exposure/infection to liver fluke, paratuberculosis, bovine diarrhoea virus and enzootic leucosis virus.

Results (NW Region only): Sixty-six percent of sampled herds (n=50) had 1 or more Bovigam positive animals (Figure 2). Overall 11% of animals sampled were bovigam test positive compared to 6% based on the SCITT.

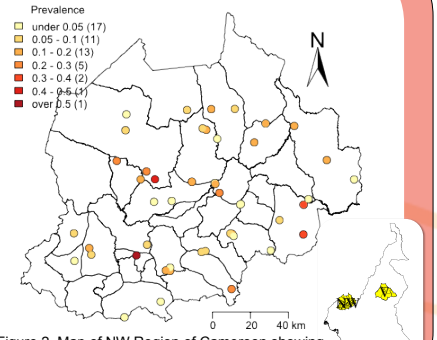
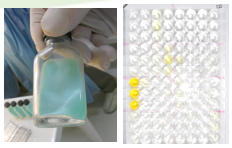


Figure 2. Map of NW Region of Cameroon showing location and within herd prevalence of bovigam positive animals (inset map location of 2 cross sectional study sites)

Laboratory Analysis

Methods: Linked clinical material and non-lesioned LNs were cultured using both L-J and liquid (MGIT) culture. All culture positive samples were screened using the Genotype® MTBC/CM/AS kits (Hain Lifescience). All M. bovis isolates will also be typed by deletion typing, spoligotyping, MIRU/VNTR and full genome sequenced.

Results (Bamenda abattoir only): the majority of positive cultures were *M. bovis* (n=31), *with one M. tuberculosis* and several NTMs including *M. fortuitum, M. gordonae, M. phlei and M. scrofulaceum*.



Putting the pieces together:

- A joint analysis of all the results will give estimates of the sensitivity and specificity of these diagnostic tests in a SSA cattle population.
- These will used to give true population based estimates of bovine TB in Cameroon with appropriate design adjustments
- Linked cultures will allow investigation of false positive or negative diagnostic test results
- Using the SCITT allowed real time feed back to farmers which was very popular.
- Additional testing for liver fluke, paratuberculosis and bovine viral diarrhoea virus will allow the impact of these co-infections to be studied.
- Using solid and liquid cultures will maximize sensitivity of culture and isolation of strains for comparison with human isolates
- Mapping and spatial analysis will be used to explore clustering of strains and transmission

Acknowledgements: The authors would like to thank MINPEA Cameroon for help carrying out this field work, the butchers and herdsmen who generously allowed their animals to be sampled and finally the Wellcome Trust (Grant No. **094945**) for funding this project.

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